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(54) Title: METHODS OF CANCER DIAGNOSIS USING A CHIMERIC TOXIN (57) Abstract <p>The present invention relates to methods for cancer diagnosis using a chimeric toxin. In particular, the invention relates to the use of a chimeric toxin composed of gonadotropin releasing hormone (GnRH) and <i>Pseudomonas</i> exotoxin A (PE) to detect a tumor-associated epitope expressed by human adenocarcinomas. Mutated GnRH-PE molecules that bind but do not kill tumor cells are exemplified.</p>		

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METHODS OF CANCER DIAGNOSIS USING A CHIMERIC TOXIN1. INTRODUCTION

The present invention relates to methods for cancer
diagnosis using a chimeric toxin. In particular, the
invention relates to the use of a chimeric toxin composed of
gonadotropin releasing hormone (GnRH) and *Pseudomonas*
exotoxin A (PE) to detect a tumor-associated epitope
expressed by human adenocarcinomas. Mutated GnRH-PE
molecules that bind but do not kill tumor cells are
exemplified.

2. BACKGROUND OF THE INVENTION

GnRH is a decapeptide produced by hypothalamic neurons
and secreted into the hypophysiportal circulation via portal
vessels. It is first synthesized as a larger precursor
protein which is processed by proteolytic cleavage and
amidation at its C-terminal glycine. GnRH stimulates
gonadotroph cells in the anterior pituitary gland to release
luteinizing hormone and follicle-stimulating hormone, thereby
regulating the hypothalamic-pituitary gonadal control of
human reproduction.

The involvement of GnRH has been implicated in certain
carcinomas, and GnRH analogues have been used in the
treatment of breast, prostatic, pancreatic, endometrial and
ovarian cancers (Kadar et al., 1988, Prostate 12:229-307).
The analogues suppressed tumor cell growth *in vitro* and *in*
vivo. In addition, GnRH binding sites have been reported in
certain solid tumors and in established cell lines (Emons et
al., 1993, J. Clin. Endocrinol. Metab. 77:1458-1464), though
preliminary results suggest that the GnRH receptor (GnRHR)
involved might differ from the previously documented receptor
(Kadar et al., 1992, Biochem. Biophys. Res. Comm. 189:289-
295).

Although GnRH binding sites have been demonstrated in
tumors, such tumors were derived mainly from hormone

dependent tissues. Recently, Nechushtan et al. reported that certain hormone non-responsive tumors such as colon carcinomas, renal cell carcinomas and hepatocellular carcinomas were susceptible to killing by a chimeric toxin, GnRH-PE (J. Biol. Chem., 1997, 272:11597). GnRH caused the
5 chimeric toxin to bind to GnRHR-expressing tumor cells, whereas PE mediated cell killing by inhibiting protein synthesis. However, prior to the present invention, it was not known whether the observed effects were due to the expression of a natural GnRHR by hormone non-responsive
10 tumors or a new epitope recognized by GnRH-PE that was distinct from that bound by GnRH.

3. SUMMARY OF THE INVENTION

The present invention relates to methods for detecting a tumor cell using a GnRH-PE chimeric toxin, and GnRH-PE
15 chimeric toxins that bind but do not kill tumor cells. In particular, it relates to the use of a GnRH-PE chimeric toxin to detect an epitope expressed by adenocarcinomas. For the practice of the invention, it is preferred that the GnRH-PE is modified to reduce its cytotoxic activities without altering its binding specificity to tumor cells. Such
20 molecules are particularly useful for the detection of tumor cells in a biological specimen and in a human subject who has cancer.

The invention is based, in part, on Applicants' discovery that two mutated recombinant chimeric toxins composed of GnRH and PE, referred to as LGnRH-PE40M and
25 LGnRH-PE66M, bind to tumor cells without killing them. Since these chimeric toxins do not bind granulosa tumor cells which express natural GnRHR recognized by GnRH, the chimeric toxins of the invention recognize a new tumor-associated epitope expressed by adenocarcinomas.

30 4. BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1A Nucleotide sequence (SEQ ID NO:1) and

and 1B. amino acid sequence (SEQ ID NO:2) of LGnRH-PE66. Amino acid residue #575 identified within a square is deleted in a mutated chimeric toxin, LGnRH-PE66M.

5 Figure 2. Nucleotide sequence (SEQ ID NO:3) and amino acid sequence (SEQ ID NO:4) of LGnRH-PE40. Amino acid residue #336 identified within a square is deleted in a mutated chimeric toxin, LGnRH-PE40M.

10 Figure 3 Mutated GnRH-PE chimeric toxins, LGnRH-PE40M and LGnRH-PE66M, did not exhibit ADP-ribosylation activities.

15 Figure 4. Mutated GnRH-PE chimeric toxins, LGnRH-PE40M and LGnRH-PE66M, did not inhibit protein synthesis in 293 renal carcinoma cells, while the non-mutated chimeric toxins showed cytotoxic activities. Inhibition of protein synthesis is used as an indication of cytotoxicity.

20 Figure 5. GnRH-PE chimeric toxins did not inhibit protein synthesis of primary cultures of granulosa tumor cells which expressed natural GnRHR.

5. DETAILED DESCRIPTION OF THE INVENTION

5.1. PRODUCTION OF GnRH-PE CHIMERIC TOXINS

25 While the GnRH-PE chimeric toxins of the present invention may be produced by chemical synthetic methods or by chemical linkage between the two moieties, it is preferred that they are produced by fusion of a coding sequence for GnRH and a coding sequence for PE under the control of a regulatory sequence which directs the expression of the fusion polynucleotide in an appropriate host cell (Nechushtan et al., 1997, J. Biol. Chem. 272:11597). The fusion of two
30 coding sequences can be achieved by methods well known in the art of molecular biology. The PE coding sequence suitable

for use in the present invention, includes but is not limited to, full length PE, partial fragments of PE such as domains II and/or III of PE, mutated PE in which amino acid residues in domain I have been altered to reduce non-specific cytotoxicity and mutated PE which has minimal cytotoxic activities (United States Patent No. 4,892,827, Lorberboum-Galski et al., 1990, J. Biol. Chem. 265:16311).

It is preferred that a fusion polynucleotide contain only the AUG translation initiation codon at the 5' end of the first coding sequence without the initiation codon of the second coding sequence to avoid the production of two encoded products. In addition, a leader sequence may be placed at the 5' end of the polynucleotide in order to target the expressed product to a specific site or compartment within a host cell to facilitate secretion or subsequent purification after gene expression. The two coding sequences can be fused directly without any linker or by using a flexible polylinker composed of the pentamer Gly-Gly-Gly-Gly-Ser (SEQ ID NO:5) repeated 1 to 3 times. Such linker has been used in constructing single chain antibodies (scFv) by being inserted between V_H and V_L (Bird et al., 1988, Science 242:423-426; Huston et al., 1988, Proc. Natl. Acad. Sci. U.S.A. 85:5979-5883). The linker is designed to enable the correct interaction between two beta-sheets forming the variable region of the single chain antibody. Other linkers which may be used include Glu-Gly-Lys-Ser-Ser-Gly-Ser-Gly-Ser-Glu-Ser-Lys-Val-Asp (SEQ ID NO:6) (Chaudhary et al., 1990, Proc. Natl. Acad. Sci. U.S.A. 87:1066-1070) and Lys-Glu-Ser-Gly-Ser-Val-Ser-Ser-Glu-Gln-Leu-Ala-Gln-Phe-Arg-Ser-Leu-Asp (SEQ ID NO:7) (Bird et al., 1988, Science 242:423-426).

5.2. EXPRESSION OF GnRH-PE CHIMERIC TOXINS

A polynucleotide which encodes a GnRH-PE chimeric toxin, mutant polypeptides, biologically active fragments of chimeric protein, or functional equivalents thereof, may be

used to generate recombinant DNA molecules that direct the expression of the chimeric toxin, mutant polypeptides, peptide fragments, or a functional equivalent thereof, in appropriate host cells. Due to the inherent degeneracy of the genetic code, other DNA sequences which encode

- 5 substantially the same or a functionally equivalent amino acid sequence, may be used in the practice of the invention for the cloning and expression of the chimeric toxin.

- Altered DNA sequences which may be used in accordance with the invention include deletions, additions or substitutions of different nucleotide residues resulting in a
- 10 sequence that encodes the same or a functionally equivalent fusion gene product. The gene product itself may contain deletions, additions or substitutions of amino acid residues within a chimeric sequence, which result in a silent change thus producing a functionally equivalent chimeric protein. Such amino acid substitutions may be made on the basis of
- 15 similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues involved. For example, negatively charged amino acids include aspartic acid and glutamic acid; positively charged amino acids include lysine, histidine and arginine; amino acids with uncharged polar head groups having similar
- 20 hydrophilicity values include the following: glycine, asparagine, glutamine, serine, threonine, tyrosine; and amino acids with nonpolar head groups include alanine, valine, isoleucine, leucine, phenylalanine, proline, methionine, tryptophan.

- The DNA sequences of the invention may be engineered in order to alter a chimeric coding sequence for a
- 25 variety of ends, including but not limited to, alterations which modify processing and expression of the gene product. For example, mutations may be introduced using techniques which are well known in the art, e.g., site-directed
- 30 mutagenesis, to insert new restriction sites, to reduce cytotoxicities, etc.

In an alternate embodiment of the invention, the coding sequence of the GnRH-PE chimeric toxin could be synthesized in whole or in part, using chemical methods well known in the art. See, for example, Caruthers et al., 1980, *Nuc. Acids Res. Symp. Ser.* 7:215-233; Crea and Horn, 1980, *Nuc. Acids Res.* 9(10):2331; Matteucci and Caruthers, 1980, *Tetrahedron Letter* 21:719; and Chow and Kempe, 1981, *Nuc. Acids Res.* 9(12):2807-2817. In addition, GnRH decapeptide and specific domains of PE can be synthesized by solid phase techniques, cleaved from the resin, and purified by preparative high performance liquid chromatography followed by chemical linkage to form a chimeric toxin (e.g., see Creighton, 1983, *Proteins Structures And Molecular Principles*, W.H. Freeman and Co., N.Y. pp. 50-60). The composition of the synthetic peptides may be confirmed by amino acid analysis or sequencing (e.g., the Edman degradation procedure; see Creighton, 1983, *Proteins, Structures and Molecular Principles*, W.H. Freeman and Co., N.Y., pp. 34-49). Alternatively, the GnRH and PE produced by synthetic or recombinant methods may be conjugated by chemical linkers according to methods well known in the art (Brinkmann and Pastan, 1994, *Biochemica et Biophysica Acta* 1198:27-45).

In order to express a biologically active GnRH-PE chimeric toxin, the nucleotide sequence coding for a chimeric toxin, or a functional equivalent, is inserted into an appropriate expression vector, i.e., a vector which contains the necessary elements for the transcription and translation of the inserted coding sequence. The chimeric toxin as well as host cells or cell lines transfected or transformed with recombinant chimeric expression vectors can be used for a variety of purposes. These include but are not limited to generating antibodies (i.e., monoclonal or polyclonal) that

bind to epitopes of the proteins to facilitate their purification.

Methods which are well known to those skilled in the art can be used to construct expression vectors containing the GnRH-PE chimeric toxin coding sequence and
5 appropriate transcriptional/translational control signals. These methods include *in vitro* recombinant DNA techniques, synthetic techniques and *in vivo* recombination/genetic recombination. See, for example, the techniques described in Sambrook et al., 1989, *Molecular Cloning A Laboratory Manual*,
10 Cold Spring Harbor Laboratory, N.Y. and Ausubel et al., 1989, *Current Protocols in Molecular Biology*, Greene Publishing Associates and Wiley Interscience, N.Y.

A variety of host-expression vector systems may be utilized to express the GnRH-PE chimeric protein coding sequence. These include but are not limited to
15 microorganisms such as bacteria transformed with recombinant bacteriophage DNA, plasmid DNA or cosmid DNA expression vectors containing the chimeric toxin coding sequence; yeast transformed with recombinant yeast expression vectors containing the chimeric toxin coding sequence; insect cell systems infected with recombinant virus expression vectors
20 (e.g., baculovirus) containing the chimeric toxin coding sequence; plant cell systems infected with recombinant virus expression vectors (e.g., cauliflower mosaic virus, CaMV; tobacco mosaic virus, TMV) or transformed with recombinant plasmid expression vectors (e.g., Ti plasmid) containing the chimeric toxin coding sequence; or animal cell systems. It
25 should be noted that since PE normally kills mammalian cells, it is preferred that the chimeric toxins of the invention be expressed in prokaryotic or lower eukaryotic cells. Section 6 illustrates that GnRH-PE chimeric toxins can be efficiently expressed in *E. coli*. However, since the mutated GnRH-PE chimeric toxins in Section 6, *infra*, do not exhibit cytotoxic

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activities towards human cells, they may be expressed in eukaryotic cells as well.

The expression elements of each system vary in their strength and specificities. Depending on the host/vector system utilized, any of a number of suitable transcription and translation elements, including constitutive and inducible promoters, may be used in the expression vector. For example, when cloning in bacterial systems, inducible promoters such as pL of bacteriophage λ , plac, ptrp, ptac (ptrp-lac hybrid promoter; cytomegalovirus promoter) and the like may be used; when cloning in insect cell systems, promoters such as the baculovirus polyhedrin promoter may be used; when cloning in plant cell systems, promoters derived from the genome of plant cells (e.g., heat shock promoters; the promoter for the small subunit of RUBISCO; the promoter for the chlorophyll α/β binding protein) or from plant viruses (e.g., the 35S RNA promoter of CaMV; the coat protein promoter of TMV) may be used; when cloning in mammalian cell systems, promoters derived from the genome of mammalian cells (e.g., metallothionein promoter) or from mammalian viruses (e.g., the adenovirus late promoter; the vaccinia virus 7.5K promoter) may be used; when generating cell lines that contain multiple copies of the chimeric DNA, SV40-, BPV- and EBV-based vectors may be used with an appropriate selectable marker.

In bacterial systems a number of expression vectors may be advantageously selected depending upon the use intended for the chimeric toxin expressed. For example, when large quantities of chimeric toxin are to be produced, vectors which direct the expression of high levels of protein products that are readily purified may be desirable. Such vectors include but are not limited to the pHL906 vector (Fishman et al., 1994, Biochem. 33:6235-6243), the *E. coli* expression vector pUR278 (Ruther et al., 1983, EMBO J. 2:1791), in which the chimeric protein coding sequence may be ligated into the vector in frame with the lacZ coding region

so that a hybrid *lacZ* protein is produced; pIN vectors (Inouye & Inouye, 1985, *Nucleic acids Res.* 13:3101-3109; Van Heeke & Schuster, 1989, *J. Biol. Chem.* 264:5503-5509); and the like.

5 An alternative expression system which could be used to express chimeric toxin is an insect system. In one such system, *Autographa californica* nuclear polyhidrosis virus (AcNPV) is used as a vector to express foreign genes. The virus grows in *Spodoptera frugiperda* cells. The chimeric toxin coding sequence may be cloned into non-essential
10 regions (for example the polyhedrin gene) of the virus and placed under control of an AcNPV promoter (for example the polyhedrin promoter). Successful insertion of the chimeric protein coding sequence will result in inactivation of the polyhedrin gene and production of non-occluded recombinant virus (i.e., virus lacking the proteinaceous coat coded for
15 by the polyhedrin gene). These recombinant viruses are then used to infect *Spodoptera frugiperda* cells in which the inserted gene is expressed. (e.g., see Smith et al., 1983, *J. Virol.* 46:584; Smith, U.S. Patent No. 4,215,051).

Specific initiation signals may also be required for efficient translation of the inserted chimeric toxin
20 coding sequence. These signals include the ATG initiation codon and adjacent sequences. In cases where the entire chimeric gene, including its own initiation codon and adjacent sequences, is inserted into the appropriate expression vector, no additional translational control signals may be needed. However, in cases where the chimeric
25 toxin coding sequence does not include its own initiation codon, exogenous translational control signals, including the ATG initiation codon, must be provided. Furthermore, the initiation codon must be in phase with the reading frame of the chimeric protein coding sequence to ensure translation of the entire insert. These exogenous translational control
30 signals and initiation codons can be of a variety of origins, both natural and synthetic. The efficiency of expression may

be enhanced by the inclusion of appropriate transcription enhancer elements, transcription terminators, etc. (see Bittner et al., 1987, Methods in Enzymol. 153:516-544).

In addition, a host cell strain may be chosen which modulates the expression of the inserted sequences, or
5 modifies and processes the gene product in the specific fashion desired. Such modifications (e.g., glycosylation) and processing (e.g., cleavage) of protein products may be important for the function of the protein. Different host cells have characteristic and specific mechanisms for the post-translational processing and modification of proteins.
10 Appropriate cell lines or host systems can be chosen to ensure the correct modification and processing of the chimeric toxin. To this end, eukaryotic host cells which possess the cellular machinery for proper processing of the primary transcript, glycosylation, and phosphorylation of the chimeric protein may be used. Such mammalian host cells
15 include but are not limited to CHO, VERO, BHK, HeLa, COS, MDCK, 293, WI38, and the like.

For long-term, high-yield production of recombinant chimeric toxins, stable expression is preferred. For example, bacterial host cells or eukaryotic cell lines which stably express the chimeric toxins may be engineered. Rather
20 than using expression vectors which contain viral origins of replication, host cells can be transformed with a chimeric coding sequence controlled by appropriate expression control elements (e.g., promoter, enhancer, sequences, transcription terminators, polyadenylation sites, etc.), and a selectable marker. Following the introduction of foreign DNA,
25 engineered cells may be allowed to grow for 1-2 days in an enriched media, and then are switched to a selective media. The selectable marker in the recombinant plasmid confers resistance to the selection and allows cells to stably integrate the plasmid into their chromosomes and grow to form foci which in turn can be cloned and expanded into cell
30 lines.

A number of selection systems may be used, including but not limited to the herpes simplex virus thymidine kinase (Wigler et al., 1977, Cell 11:223), hypoxanthine-guanine phosphoribosyltransferase (Szybalska & Szybalski, 1962, Proc. Natl. Acad. Sci. USA 48:2026), and
5 adenine phosphoribosyltransferase (Lowy et al., 1980, Cell 22:817) genes can be employed in tk⁻, hgp⁻ or ap⁻ cells, respectively. Also, antimetabolite resistance can be used as the basis of selection for *dhfr*, which confers resistance to methotrexate (Wigler et al., 1980, Natl. Acad. Sci. USA
10 77:3567; O'Hare et al., 1981, Proc. Natl. Acad. Sci. USA 78:1527); *gpt*, which confers resistance to mycophenolic acid (Mulligan & Berg, 1981, Proc. Natl. Acad. Sci. USA 78:2072); *neo*, which confers resistance to the aminoglycoside G-418 (Colberre-Garapin et al., 1981, J. Mol. Biol. 150:1); and
15 *hygro*, which confers resistance to hygromycin (Santerre et al., 1984, Gene 30:147) genes. Additional selectable genes have been described, namely *trpB*, which allows cells to utilize indole in place of tryptophan; *hisD*, which allows cells to utilize histinol in place of histidine (Hartman &
20 Mulligan, 1988, Proc. Natl. Acad. Sci. USA 85:8047); and *ODC* (ornithine decarboxylase) which confers resistance to the ornithine decarboxylase inhibitor, 2-(difluoromethyl)-DL-ornithine, DFMO (McConlogue L., 1987, In: Current Communications in Molecular Biology, Cold Spring Harbor Laboratory ed.).

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5.3. PROTEIN PURIFICATION

The GnRH-PE chimeric toxins of the invention can be purified by art-known techniques such as high performance liquid chromatography, ion exchange chromatography, gel electrophoresis, affinity chromatography and the like. The
30 actual conditions used to purify each protein will depend, in part, on factors such as net charge, hydrophobicity,

hydrophilicity, etc., and will be apparent to those having skill in the art.

For affinity chromatography purification, any antibody which specifically binds GnRH, PE or a conformational epitope created by the fusion of GnRH and PE
5 may be used. For the production of antibodies, various host animals, including but not limited to rabbits, mice, rats, etc., may be immunized by injection with GnRH-PE chimeric toxin or a portion thereof. The protein may be attached to a suitable carrier, such as bovine serum albumin (BSA); by means of a side chain functional group or linkers attached to
10 a side chain functional group. Various adjuvants may be used to increase the immunological response, depending on the host species, including but not limited to, Freund's (complete and incomplete), mineral gels such as aluminum hydroxide, surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, keyhole limpet
15 hemocyanin, dinitrophenol, and potentially useful human adjuvants such as BCG (bacilli Calmette-Guerin) and *Corynebacterium parvum*.

Monoclonal antibodies to GnRH-PE may be prepared using any technique which provides for the production of antibody molecules by continuous cell lines in culture.
20 These include but are not limited to the hybridoma technique originally described by Koehler and Milstein (1975, Nature 256:495-497). In addition, techniques developed for the production of "chimeric antibodies" (Morrison et al., 1984, Proc. Natl. Acad. Sci. U.S.A. 81:6851-6855; Neuberger et al.,
25 1984, Nature 312:604-608; Takeda et al., 1985, Nature 314:452-454) by splicing the genes from a mouse antibody molecule of appropriate antigen specificity together with genes from a human antibody molecule of appropriate biological activity can be used. Alternatively, techniques described for the production of single chain antibodies (U.S.
30 Patent No. 4,946,778) can be adapted to produce GnRH-PE-

specific single chain antibodies for protein purification and detection.

5.4. CANCER DIAGNOSIS USING GnRH-PE CHIMERIC TOXINS

5 The GnRH-PE chimeric toxins of the invention may be used to detect human tumors *in vitro* and *in vivo*. It is preferred that such toxins be mutated to abrogate their cytotoxic properties without affecting their binding specificity for tumor cells. Two examples of such GnRH-PE are illustrated in Section 6, *infra*. The GnRH-PE chimeric
10 toxins of the invention may be used to detect an epitope expressed by a wide variety of human adenocarcinomas, including but not limited to, colon adenocarcinoma, breast adenocarcinoma, lung adenocarcinoma, ovarian adenocarcinoma, endometrial adenocarcinoma, kidney adenocarcinoma, liver adenocarcinoma, prostate adenocarcinoma, stomach
15 adenocarcinoma, cervical adenocarcinoma, gall bladder adenocarcinoma and pancreatic adenocarcinoma. The chimeric toxins of the invention are particularly useful in differentiating adenocarcinomas from non-adenocarcinomas and normal cells that express the natural GnRHR.

20 5.4.1. IN VITRO DIAGNOSTIC APPLICATIONS

The GnRH-PE chimeric toxins of the present invention can be used to detect cancer cells in a biological specimen such as histological and cytological specimens, and, in particular, to distinguish malignant tumors from normal tissues and non-malignant tumors for determination of
25 surgical margin and an improved histological characterization of poorly differentiated tumors. Tissue specimens may be stained by the chimeric toxins and their binding detected by a secondary antibody specific for a portion of the chimeric toxin. The secondary antibody is conjugated to a detectable label such as a radioisotope, an enzyme such as peroxidase
30 and alkaline phosphatase, an ultrasonic probe, a nuclear magnetic resonance (NMR) probe, and the like.

In addition, immunofluorescence techniques can use GnRH-PE to examine human tissue, cell and bodily fluid specimens. In a typical protocol, slides containing cryostat sections of frozen, unfixed tissue biopsy samples or cytological smears are air dried, formalin or acetone fixed, and incubated with the GnRH-PE in a humidified chamber' at room temperature.

The slides are then washed and further incubated with a preparation of a secondary antibody directed against GnRH-PE. The secondary antibody is tagged with a compound such as rhodamine, phycoerythrin or fluorescein isothiocyanate, that fluoresces at a particular wavelength. The staining pattern and intensities within the sample are then determined by fluorescent light microscopy and optionally photographically recorded.

In another embodiment, computer enhanced fluorescence image analysis or flow cytometry can be used to examine tissue specimens or exfoliated cells, i.e., single cell preparations from aspiration biopsies of tumors using GnRH-PE. The GnRH-PE chimeric toxins of the invention are particularly useful in quantitation of live tumor cells, i.e., single cell preparations from aspiration biopsies of adenocarcinomas by computer enhanced fluorescence image analyzer or with a flow cytometer. The percent GnRH-PE-bound cell population, alone or in conjunction with determination of the DNA ploidy of these cells, may, additionally, provide very useful prognostic information by providing an early indicator of disease progression.

The use of GnRH-PE can be extended to the screening of human biological fluids for the presence of the specific antigenic determinants recognized. In vitro immunoserological evaluation of biological fluids withdrawn from patients thereby permits non-invasive diagnosis of cancers. By way of illustration, human bodily fluids such as whole blood, pleural effusion fluid, cerebral spinal fluid, synovial fluid, prostatic fluid, seminal fluid or urine can

be taken from a patient and assayed for the specific epitope, either as released antigen or membrane-bound on cells in the sample fluid, using GnRH-PE in standard radioimmunoassays or enzyme-linked immunoassays, competitive binding enzyme-linked immunoassays, dot blot or Western blot, or other assays known
5 in the art.

Kits containing GnRH-PE can be prepared for *in vitro* diagnosis, prognosis and/or monitoring adenocarcinomas by the immunohistological, immunocytological and immunoserological methods described above. The components of
10 the kits can be packaged either in aqueous medium or in lyophilized form. When the GnRH-PE is used in the kits in the form of conjugates in which a label moiety is attached, such as an enzyme or a radioactive metal ion, the components of such conjugates can be supplied either in fully conjugated form, in the form of intermediates or as separate moieties to
15 be conjugated by the user of the kit.

A kit may comprise a carrier being compartmentalized to receive in close confinement therein one or more container means or series of container means such as test tubes, vials, flasks, bottles, syringes, or the like. A first of said container means or series of container means
20 may contain GnRH-PE. A second container means or series of container means may contain a label or linker-label intermediate capable of binding to GnRH-PE.

5.4.2. IN VIVO DIAGNOSTIC APPLICATIONS

GnRH-PE chimeric toxins are also useful for
25 targeting adenocarcinoma cells *in vivo*. They can be used for tumor localization in the detection and monitoring of primary tumors as well as metastases, especially lymph nodes. Primary evaluation of the extent of tumor spread may influence the choice of therapeutic modalities. Continued monitoring of residual tumors may also contribute to better
30 surveillance and early initiation of salvage therapy. Tagged GnRH-PE may also be used intraoperatively for better

debulking of a tumor, and minimizes normal tissue destruction such as lymph nodes. For these *in vivo* applications, it is preferred that highly purified GnRH-PE be used.

For *in vivo* detection and/or monitoring of adenocarcinomas, the purified GnRH-PE can be covalently
5 attached, either directly or via a linker, to a compound which serves as a reporter group to permit imaging of specific tissues or organs following administration and localization of the conjugates or complexes. A variety of different types of substances can serve as the reporter
10 group, including such as radiopaque dyes, radioactive metal and non-metal isotopes, fluorogenic compounds, fluorescent compounds, positron emitting isotopes, non-paramagnetic metals, etc.

Kits for use with such *in vivo* tumor localization methods containing GnRH-PE (or fragments thereof) conjugated
15 to any of the above types of substances can be prepared. The components of the kits can be packaged either in aqueous medium or in lyophilized form. When the chimeric toxins are used in the kits in the form of conjugates in which a label is attached, the components of such conjugates can be supplied either in fully conjugated form, in the form of
20 intermediates or as separate moieties to be conjugated by the user of the kit.

6. **EXAMPLE: MUTATED GnRH-PE CHIMERIC TOXINS**
BOUND BUT DID NOT KILL TUMOR CELLS

6.1. **MATERIALS AND METHODS**

25 6.1.1. **CONSTRUCTION OF GnRH-PE CHIMERIC TOXINS**

A plasmid vector carrying a full length PE gene (pJY3A1136-1,3) (Chaudhary et al., 1990, J. Biol. Chem. 265:16306-16310; Neshushtan et al., 1997, J. Biol. Chem. 272:11597) was cut with NdeI and HindIII. A 36 base pair
30 (bp) synthetic oligomer flanked by NdeI (5' end) and HindIII (3' end) restriction sites was ligated to the vector. This

oligomer insert contained a GnRH coding sequence in which the encoded amino acid at residue #6 was tryptophan instead of glycine. In addition, a sequence encoding a linker Gly-Gly-Gly-Gly-Ser (SEQ ID NO:5) repeated twice was placed between the GnRH coding sequence and the PE coding sequence. The
5 resultant plasmid encoded a chimeric toxin, LGnRH-PE66, and it was confirmed by restriction endonuclease digestion and DNA sequence analysis (Figure 1A and 1B).

In order to produce a second chimeric toxin, LGnRH-PE40, the plasmid vector encoding LGnRH-PE66 was digested with NdeI and BamHI and ligated to a NdeI-BamHI 750 bp
10 fragment obtained from the plasmid PHL-906 (Fishman et al., 1994, Biochemistry 33:6235-6243) along with the 36 bp synthetic oligomer consisting of the GnRH coding sequence with tryptophan replacing glycine at the sixth amino acid position. A sequence encoding the above linker was again
15 placed between the GnRH coding sequence and the PE coding sequence. The resultant plasmid encoded a chimeric toxin, LGnRH-PE40, and it was confirmed by restriction endonuclease digestion and DNA sequence analysis (Figure 2). The toxin encoded by this plasmid consisted of domains II and III of the full-length PE.

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6.1.2. GENERATION OF MUTATED
GnRH-PE CHIMERIC TOXINS

In order to construct GnRH-PE chimeric toxins that were not cytotoxic to human cells, the region in the two aforementioned plasmids that encoded 122 amino acids at the
25 C-terminal end of PE of LGnRH-PE66 and LGnRH-PE40 was excised with BamHI and EcoRI and replaced with a corresponding fragment which contained a deletion of a single codon encoding the amino acid at position 553 of the native PE molecule (Figures 1A, 1B and 2) (Fishman et al., 1997, Eur. J. Immunol. 27:486; Lukoc et al., 1988, Infect. Immun.
30 56:3095). The mutated chimeric toxins are referred to as LGnRH-PE66M and LGnRH-PE40M, respectively.

6.1.3. EXPRESSION OF GnRH-PE CHIMERIC TOXINS

The plasmids, pVM1 and pVM2, encoding the mutated GnRH-PE chimeric toxins, LGnRH-PE66M and LGnRH-PE40M, respectively, were expressed in *E. coli* strain BL21 (λ DE3).
5 The plasmids that encoded LGnRH-PE40 and LGnRH-PE66 were also expressed in the same bacteria. The plasmids were transferred into *E. coli* and the cells were grown in medium containing ampicillin. After reaching an A_{600} value of 1.5-1.7, the cultures were induced at 37°C with 1 mM isopropyl-1-thio- β -D-galactopyranoside. The cells were collected by
10 centrifugation and the pellet was stored at -70°C for several hours.

A pellet of expressing cells was suspended in lysis buffer (50 mM Tris-HCl at pH 8.0, 1mM EDTA containing 0.2 mg/ml lysosyme), sonicated (three 30 second bursts) and centrifuged at 30,000xg for 30 min. The supernatant (soluble
15 fraction) was removed and kept for analysis. The pellet (insoluble fraction) was denatured in extraction buffer (6 M guanidinium-HCl, 0.1 M Tris-HCl, pH 8.6, 1mM EDTA, 0.05 M NaCl, and 10 mM dithiothreitol) and stirred for 30 min at 4°C. The suspension was cleared by centrifugation at 30000xg for 15 min and the pellet discarded. The supernatant was
20 then dialyzed against 0.1 M Tris-HCl pH 8.0, 1mM EDTA, 0.25mM NaCl, and 0.25mM L-arginine for 16 hours. The dialyzate was centrifuged at 15000xg for 15 min and the resulting supernatant (refolding fraction) was used as a source of the GnRH-PE chimeric toxins.

Analysis of the fraction by SDS/PAGE revealed a
25 major band corresponding to the chimeric toxin. Immunoblotting with polyclonal antibodies against PE confirmed the production of GnRH-PE chimeric toxins.

6.1.4. PURIFICATION OF RECOMBINANT GnRH-PE CHIMERIC TOXINS

30 The refolded protein fractions were diluted with TE20 buffer (20mM Tris, pH 8.0, 1mM EDTA). DEAE Sepharose

(Pharmacia, Sweden) was added and stirred for half an hour at 4°C before being packed into a column. Washing of the column was done with 80mM NaCl or 50mM NaCl in TE20 buffer.

Elution of protein was performed with the linear gradient of 2 x 200ml of 0.08-0.35M NaCl in TE20 (20mM Tris pH 8.0, 1mM EDTA) buffer. The peak fractions were pooled, dialyzed against phosphate saline buffer and kept in aliquots at -20°C.

6.2. RESULTS

A recombinant GnRH-PE chimeric toxin, LGnRH-PE66, was produced by fusion of a GnRH coding sequence and a PE coding sequence with the insertion of a linker between the two moieties. A second GnRH-PE chimeric toxin, LGnRH-PE40, was produced in a similar manner except that only domains II and III of PE was encoded by the toxin coding sequence. In addition, the coding sequences of these two chimeric toxins were mutated to result in a single amino acid deletion in the PE portion. The mutated chimeric toxins were also expressed as recombinant proteins.

The four GnRH-PE chimeric toxins were purified from *E. coli* lysates and refolded. Since PE kills eukaryotic cells by inactivating elongation factor 2 through ADP-ribosylation during protein synthesis, the four forms of GnRH-PE chimeric toxins were tested in a cell free assay for their enzymatic activities in ADP-ribosylation (Chung and Collier, 1977, J. Infect. Immun. 16:832-841). While the two non-mutated GnRH-PE chimeric toxins, LGnRH-PE40 and LGnRH-PE66, exhibited ADP-ribosylation activities, the mutated chimeric toxins, LGnRH-PE40M and LGnRH-PE66M, were completely inactive in the same assay (Figure 3). Thus, a single amino acid substitution in PE abrogated the enzymatic activities of the chimeric toxins.

In addition, all four GnRH-PE chimeric toxins were tested for their ability to kill 293 renal adenocarcinoma cells. It was shown that only the non-mutated chimeric

toxins showed dose-dependent inhibition of protein synthesis in the target cells (Figure 4). However, when the chimeric toxins were incubated with the same target cells and their binding was detected by a labeled anti-PE antibody and FACS analysis, all four toxins were able to bind renal carcinoma
5 cells with no binding to control T24A bladder carcinoma cells. Therefore, while the mutated GnRH-PE chimeric toxins were not able to kill target cells, they retained the ability to bind to tumor cells. Such non-cytotoxic chimeric toxins are particularly useful for use in cancer diagnosis *in vitro* and *in vivo*.

10 Primary granulosa tumor cells were obtained and shown to express GnRHR by PCR using primers corresponding to specific portions of the GnRHR. The PCR product in granulosa cells was the same size as that obtained from pituitary cells which expressed natural GnRHR. In contrast, GnRHR-negative
15 cells such as normal human lymphocytes did not produce a detectable PCR product. Notwithstanding their expression of natural GnRHR, the granulosa cells were not susceptible to killing by any of the four GnRH-PE chimeric toxins, indicating that the chimeric toxins bind to a new epitope expressed by adenocarcinoma cells that is distinct from that
20 bound by GnRH itself (Figure 5).

The present invention is not to be limited in scope by the exemplified embodiments which are intended as
illustrations of single aspects of the invention and any
25 sequences which are functionally equivalent are within the scope of the invention. Indeed, various modifications of the invention in addition to those shown and described herein will become apparent to those skilled in the art from the foregoing description and accompanying drawings. Such
modifications are intended to fall within the scope of the
30 appended claims.

All publications cited herein are incorporated by reference in their entirety.

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WHAT IS CLAIMED IS

1. A method for detecting a tumor cell in a biological specimen, comprising contacting the biological specimen with a chimeric toxin which comprises gonadotropin releasing hormone and *Pseudomonas* exotoxin A, and detecting chimeric toxin-bound cells in the specimen.

2. The method of Claim 1 in which biological specimen contains adenocarcinoma cells.

3. The method of Claim 2 in which the adenocarcinoma cells are selected from a group consisting of colon adenocarcinoma, breast adenocarcinoma, lung adenocarcinoma, ovarian adenocarcinoma, endometrial adenocarcinoma, kidney adenocarcinoma, liver adenocarcinoma, prostate adenocarcinoma, stomach adenocarcinoma, cervical adenocarcinoma, gall bladder adenocarcinoma and pancreatic adenocarcinoma.

4. The method of Claim 1 in which the *Pseudomonas* exotoxin is a full-length toxin.

5. The method of Claim 1 in which the *Pseudomonas* exotoxin contains only domains II and III of a full-length toxin.

6. The method of Claim 1 in which the chimeric toxin comprises the amino acid sequence as shown in SEQ ID NO:2.

7. The method of Claim 6 in which the chimeric toxin is encoded by a polynucleotide which comprises the nucleotide sequence as shown in SEQ ID NO:1.

8. The method of Claim 1 in which the chimeric toxin comprises the amino acid sequence of SEQ ID NO:4.

9. The method of Claim 8 in which the chimeric toxin is encoded by a polynucleotide which comprises the
5 nucleotide sequence as shown in SEQ ID NO:3.

10. The method of Claim 1 in which the *Pseudomonas* exotoxin is rendered non-cytotoxic.

10 11. The method of Claim 10 in which the *Pseudomonas* exotoxin is rendered non-cytotoxic by deleting an amino acid residue.

12. The method of Claim 1 in which the chimeric toxin comprises the amino acid sequence as shown in SEQ ID
15 NO:2 wherein amino acid residue #575 is deleted.

13. The method of Claim 12 in which the chimeric toxin is encoded by a polynucleotide which comprises the nucleotide sequence as shown as SEQ ID NO:1 wherein nucleotides #1822-1824 are deleted.

20 14. The method of Claim 1 in which the chimeric toxin comprises the amino acid sequence as shown in SEQ ID NO:4 wherein amino acid residue #336 is deleted.

25 15. The method of Claim 14 in which the chimeric toxin is encoded by a polynucleotide which comprises the nucleotide sequence as shown in SEQ ID NO:3 wherein nucleotides #1105-1107 are deleted.

16. The method of Claim 1 in which the chimeric toxin is conjugated to a detectable label.

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17. The method of Claim 16 in which the detectable label is a radioisotope, a fluorescent dye, an enzyme, an ultrasonic probe or a NMR probe.

18. The method of Claim 1 in which the biological
5 specimen is a biopsy specimen.

19. The method of Claim 1 in which the biological specimen is a bodily fluid.

20. The method of Claim 19 in which the bodily
10 fluid is whole blood.

21. The method of Claim 19 in which the bodily fluid is pleural effusion fluid.

22. The method of Claim 19 in which the bodily
15 fluid is urine.

23. A method of detecting a tumor cell in a human subject, comprising administering to the subject a chimeric toxin which comprises gonadotropin releasing hormone and *Pseudomonas* exotoxin A, and detecting chimeric toxin-bound
20 cells in the subject.

24. The method of Claim 23 in which the subject has adenocarcinoma.

25. The method of Claim 24 in which the
adenocarcinoma is selected from a group consisting of colon adenocarcinoma, breast adenocarcinoma, lung adenocarcinoma, ovarian adenocarcinoma, endometrial adenocarcinoma, kidney adenocarcinoma, liver adenocarcinoma, prostate adenocarcinoma, stomach adenocarcinoma, cervical
adenocarcinoma, gall bladder adenocarcinoma and pancreatic
30 adenocarcinoma.

26. The method of Claim 1 in which the *Pseudomonas* exotoxin is rendered non-cytotoxic.

27. The method of Claim 26 in which the
5 *Pseudomonas* exotoxin is rendered non-cytotoxic by deleting an amino acid residue.

28. The method of Claim 1 in which the chimeric toxin comprises the amino acid sequence as shown in SEQ ID NO:2 wherein amino acid residue #575 is deleted.

10 29. The method of Claim 28 in which the chimeric toxin is encoded by a polynucleotide which comprises the nucleotide sequence as shown in SEQ ID NO:1 wherein nucleotides #1822-1824 are deleted.

15 30. The method of Claim 1 in which the chimeric toxin comprises the amino acid sequence as shown in SEQ ID NO:4 wherein amino acid residue #336 is deleted.

31. The method of Claim 30 in which the chimeric toxin is encoded by a polynucleotide which comprises the
20 nucleotide sequence as shown in SEQ ID NO:3 wherein nucleotides #1105-1107 are deleted.

32. The method of Claim 23 in which the chimeric toxin is conjugated to a detectable label.

25 33. The method of Claim 32 in which the detectable label is a radioisotope, a fluorescent dye, an enzyme, an ultrasonic probe or a NMR probe.

34. A chimeric toxin comprising gonadotropin releasing hormone and *Pseudomonas* exotoxin A, wherein the
30 toxin binds but does not kill tumor cells.

35. The chimeric toxin of Claim 34 which comprises the amino acid sequence as shown in SEQ ID NO:2 wherein the amino acid residue #575 is deleted.

5 36. The chimeric toxin of Claim 35 which is encoded by a polynucleotide which comprises the nucleotide sequence as shown in SEQ ID NO:1 wherein nucleotides #1822-1824 are deleted.

37. The chimeric toxin of Claim 34 which comprises the amino acid sequence as shown in SEQ ID NO:4 wherein the
10 amino acid residue #336 is deleted.

38. The chimeric toxin of Claim 37 which is encoded by a polynucleotide which comprises the nucleotide sequence as shown in SEQ ID NO:3 wherein nucleotides #1105-1107 are deleted.
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1/7

100/1	130/11
ATG gag cac tgg tcc tat tgg ctg cgc cct	gga gaa gct gga gga gga gga lcc gga gga
MET glu his trp ser tyr trp leu arg pro	gly glu ala gly gly gly gly ser gly gly
160/21	190/31
gga gga tcc ggt caa gct ttc gac ctc tgg aac gaa tgc gcc aac gcc tgc gtg ctc gac	
gly gly ser gly gln ala phe asp leu trp	asn glu cys ala lys ala cys val leu asp
220/41	250/51
ctc aag gac ggc gtg cgt tcc agc cgc atg agc gtc gac ccg gcc atc gcc gac acc aac	
leu lys asp gly val arg ser ser arg met	ser val asp pro ala ile ala asp thr asn
280/61	310/71
ggc cag ggc gtg ctg cac tac tcc atg gtc ctg gag ggc ggc aac gac gcg ctc gag ctg	
gly gln gly val leu his tyr ser met val leu glu gly gly asn asp ala leu glu leu	
340/81	370/91
gcc atc gac aac gcc ctc agc atc acc agc gac ggc ctg acc atc cgc ctc gaa ggc ggc	
ala ile asp asn ala leu ser ile thr ser	asp gly leu thr ile arg leu glu gly gly
400/101	430/111
gtc gag ccg aac aag ccg ctg cgc tac agc	tac acg cgc cag gcg cgc ggc agg tgg tgc
val glu pro asn lys pro leu arg tyr ser	tyr thr arg gln ala arg gly arg trp ser
460/121	490/131
ctg aac tgg ctg gta ccg atc ggc cac gag aag ccc tgc aac atc aag gtg ttc atc cac	
leu asn trp leu val pro ile gly his glu	lys pro ser asn ile lys val phe ile his
520/141	550/151
gaa ctg aac gcc ggc aac cag ctc agc cac atg tgc ccg atc tac acc atc gag atg ggc	
glu leu asn ala gly asn gln leu ser his	met ser pro ile tyr thr ile glu met gly
580/161	610/171
gac gag ttg ctg gcg aag ctg gcg cgc gat gcc acc ttc ttc gtc agg gcg cac gag agc	
asp glu leu leu ala lys leu ala arg asp	ala thr phe phe val arg ala his glu ser
640/181	670/191
aac gag atg cag ccg acg ctc gcc atc agc cat gcc ggg gtc agc gtg gtc atg gcc cag	
asn glu met gln pro thr leu ala ile ser	his ala gly val ser val val met ala gln
700/201	730/211
acc cag ccg cgc cgg gaa aag cgc tgg agc gaa tgg gcc agc ggc aag gtg ttg tgc ctg	
thr gln pro arg arg glu lys arg trp ser	glu trp ala ser gly lys val leu cys leu
760/221	790/231
ctc gac ccg ctg gac ggg gtc tac aac tac ctc gcc cag caa cgc tgc aac ctc gac gat	
leu asp pro leu asp gly val tyr asn tyr	leu ala gln gln arg cys asn leu asp asp
820/241	850/251
acc tgg gaa ggc aag atc tac cgg gtg ctc gcc ggc aac ccg gcg aag cat gac ctg gac	
thr trp glu gly lys ile tyr arg val leu	ala gly asn pro ala lys his asp leu asp
880/261	910/271
atc aac ccc acg gtc atc agt gaa gag ctg gag ttt ccc gag ggc ggc agc ctg gcc gcg	
ile lys pro thr val ile ser glu glu leu	glu phe pro glu gly gly ser leu ala ala
940/281	970/291
ctg acc gcg cac cag gct tgc cac ctg ccg ctg gag act ttc acc cgt cat cgc cag ccg	
leu thr ala his gln ala cys his leu pro leu glu thr phe thr arg his arg gln pro	

FIG. 1A

SUBSTITUTE SHEET (RULE 26)

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1000/301 1030/311
 cgc ggc lgg gaa caa ctg gag cag tgc ggc tat ccg gtg cag cgg ctg gtc gcc ctc tac
 arg gly trp glu gln leu glu gln cys gly tyr pro val gln arg leu val ala leu tyr
 1060/321 1090/331
 ctg gcg gcg cgg ctg tgc tgg aac cag gtc gac cag gtg atc cgc aac gcc ctg gcc agc
 leu ala ala arg leu ser trp asn gln val asp gln val ile arg asn ala leu ala ser
 1120/341 1150/351
 ccc ggc agc ggc ggc gac ctg ggc gaa gcg atc cgc gag cag ccg gag cag gcc cgt ctg
 pro gly ser gly gly asp leu gly glu ala ile arg glu gln pro glu gln ala arg leu
 1180/361 1210/371
 gcc ctg acc ctg gcc gcc gcc gag agc gag cgc ttc gtc cgg cag ggc acc ggc aac gac
 ala leu thr leu ala ala ala glu ser glu arg phe val arg gln gly thr gly asn asp
 1240/381 1270/391
 gag gcc ggc gcg gcc aac gcc gac gtg gtg agc ctg acc tgc ccg gtc gcc gcc ggt gaa
 glu ala gly ala ala asn ala asp val val ser leu thr cys pro val ala ala gly glu
 1300/401 1330/411
 tgc gcg ggc ccg gcg gac agc ggc gac gcc ctg ctg gag gcg aac tat ccc act ggc gcg
 cys ala gly pro ala asp ser gly asp ala leu leu glu ala asn tyr pro thr gly ala
 1360/421 1390/431
 gag ttc ctc ggc gac ggc ggc gac gtc agc ttc agc acc cgc ggc acc cag aac tgg acc
 glu phe leu gly asp gly gly asp val ser phe ser thr arg gly thr gln asn trp thr
 1420/441 1450/451
 glg gag cgg ctg ctc cag gcg cac cgc caa ctg gag gag cgc gcc tat glg ttc gtc gcc
 val glu arg leu leu gln ala his arg gln leu glu glu arg gly tyr val phe val gly
 1480/461 1510/471
 tac cac ggc acc ttc ctc gaa gcg gcg caa agc atc gtc ttc ggc ggg glg cgc gcg cgc
 tyr his gly thr phe leu glu ala ala gln ser ile val phe gly gly val arg ala arg
 1540/481 1570/491
 agc cag gac ctc gac gcg atc tgg cgc ggt ttc tat atc gcc ggc gat ccg gcg ctg gcc
 ser gln asp leu asp ala ile trp arg gly phe tyr ile ala gly asp pro ala leu ala
 1600/501 1630/511
 tac ggc tac gcc cag gac cag gaa ccc gac gca cgc ggc cgg atc gcg aac ggt gcc ctg
 tyr gly tyr ala gln asp gln glu pro asp ala arg gly arg ile arg asn gly ala leu
 1660/521 1690/531
 ctg cgg gtc tat gtg ccg cgc tgc agc ctg ccg ggc ttc tac cgc acc agc ctg acc ctg
 leu arg val tyr val pro arg ser ser leu pro gly phe tyr arg thr ser leu thr leu
 1720/541 1750/551
 gcc gcg ccg gag gcg gcg ggc gag gtc gaa cgg ctg atc ggc cat ccg ctg ccg ctg cgc
 ala ala pro glu ala ala gly glu val glu arg leu ile gly his pro leu pro leu arg
 1780/561 1810/571
 ctg gac gcc atc acc ggc ccc gag gag gaa ggc ggg cgc ctg gag acc att ctc ggc tgg
 leu asp ala ile thr gly pro glu glu glu gly gly arg leu glu thr ile leu gly trp
 1840/581 1870/591
 ccg ctg gcc gag cgc acc gtg gtg att ccc tgc gcg atc ccc acc gac ccg cgc aac gtc
 pro leu ala glu arg thr val val ile pro ser ala ile pro thr asp pro arg asn val

FIG. 1B

SUBSTITUTE SHEET (RULE 26)

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1900/601

1930/611

ggc ggc gac ctc gac ccg tcc agc atc ccc gac aag gaa cag gcg atc agc gcc ctg ccg
gly gly asp leu asp pro ser ser ile pro asp lys glu gln ala ile ser ala leu pro

1960/621

1990/631

gac tac gcc agc cag ccc ggc aaa ccg ccg cgc gag gac ctg aag too
asp tyr ala ser gln pro gly lys pro pro arg glu asp leu lys OCH

FIG.1C

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100/1 130/11
 ATG gag cac tgg tcc tat tgg ctg cgc cct gga gaa gct gga gga gga gga tcc gga gga
 Met glu his trp ser tyr trp leu arg pro gly glu ala gly gly gly gly ser gly gly
 160/21 190/31
 gga gga tcc ggt cAA GCT TTT GTT AAC GCC CAT ATG GCC GAA GAG GGC GGC AGC CTG GCC
 gly gly ser gly gln ala phe val asn ala his met ala glu glu gly gly ser leu ala
 220/41 250/51
 GCG CTG ACC GCG CAC CAG GCT TGC CAC CTG CCG CTG GAG ACT TTC ACC CGT CAT CGC CAG
 ala leu thr ala his gln ala cys his leu pro leu glu thr phe thr arg his arg gln
 280/61 310/71
 CCG CGC GGC TGG GAA CAA CTG GAG CAG TGC GGC TAT CCG GTG CAG CCG CTG GTC GCC CTC
 pro arg gly trp glu gln leu glu gln cys gly tyr pro val gln arg leu val ala leu
 340/81 370/91
 TAC CTG GCG GCG CCG CTG TCG TGG AAC CAG GTC GAC CAG GTG ATC CGC AAC GCC CTG GCC
 tyr leu ala ala arg leu ser trp asn gln val asp gln val ile arg asn ala leu ala
 400/101 430/111
 AGC CCC GGC AGC GGC GGC GAC CTG GGC GAA GCG ATC CGC GAG CAG CCG GAG CAG GCC CGT
 ser pro gly ser gly gly asp leu gly glu ala ile arg glu gln pro glu gln ala arg
 460/121 490/131
 CTG GCC CTG ACC CTG GCC GCC GCC GAG AGC GAG CGC TTC GTC CCG CAG GGC ACC GGC AAC
 leu ala leu thr leu ala ala ala glu ser glu arg phe val arg gln gly thr gly asn
 520/141 550/151
 GAC GAG GCC GGC GCG GCC AAG GCC GAC GTG GTG AGC CTG ACC TGC CCG GTC GCC GCC GGT
 asp glu ala gly ala ala asn ala asp val val ser leu thr cys pro val ala ala gly
 580/161 610/171
 GAA TGC GCG GGC CCG GCG GAC AGC GGC GAC GCC CTG CTG GAG CGC AAC TAT CCC ACT GGC
 glu cys ala gly pro ala asp ser gly asp ala leu leu glu arg asn tyr pro thr gly
 640/181 670/191
 GCG GAG TTC CTC GGC GAC GGC GGC GAC GTC AGC TTC AGC ACC CCG GGC ACG CAG AAC TGG
 ala glu phe leu gly asp gly gly asp val ser phe ser thr arg gly thr gln asn trp
 700/201 730/211
 ACG GTG GAG CCG CTG CTC CAG GCG CAC GCG GAA CTG GAG GAG CGC GGC TAT GTG TTC GTC
 thr val glu arg leu leu gln ala his arg gln leu glu glu arg gly tyr val phe val
 760/221 790/231
 GGC TAC CAC GGC ACC TTC CTC GAA GCG GCG CAA AGC ATC GTC TTC GGC GGC GTG CGC GCG
 gly tyr his gly thr phe leu glu ala ala gln ser ile val phe gly gly val arg ala
 820/241 850/251
 CGC AGC CAG GAC CTC GAC GCG ATC TGG CGC GGT TTC TAT ATC GCC GGC GAT CCG GCG CTG
 arg ser gln asp leu asp ala ile trp arg gly phe tyr ile ala gly asp pro ala leu
 880/261 910/271
 GCC TAC GGC TAC GCC CAG GAC CAG GAA CCC GAC GCA CGC GGC CCG ATC CGC AAC GGT GCC
 ala tyr gly tyr ala gln asp gln glu pro asp ala arg gly arg ile arg asn gly ala

FIG.2A

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940/281	970/291
CTG CTG CCG GTC TAT GTG CCG CCG TCG AGC CTG CCG GGC TTC TAC CCG ACC AGC CTG ACC	
leu leu arg val tyr val pro arg ser ser leu pro gly phe tyr arg thr ser leu thr	
1000/301	1030/311
CTG GCC CCG CCG GAG GCG GCG GGC GAG GTC GAA CCG CTG ATC GGC CAT CCG CTG CCG CTG	
leu ala ala pro glu ala ala gly glu val glu arg leu ile gly his pro leu pro leu	
1060/321	1090/331
CGC CTG GAC GCC ATC ACC GGC CCC GAG GAG GAA GGC GGG CCG CTG	GAG ACC ATT CTC GGC
arg leu asp ala ile thr gly pro glu glu glu gly gly arg leu	glu thr ile leu gly
1120/341	1150/351
TGG CCG CTG GCC GAG CCG ACC GTG GTG ATT CCC TCG GCG ATC CCC ACC GAC CCG CCG AAC	
trp pro leu ala glu arg thr val val ile pro ser ala ile pro thr asp pro arg asn	
1180/361	1210/371
GTC GGC GGC GAC CTC GAC CCG TCC AGC ATC CCC GAC AAG GAA CAG GCG ATC AGC GCC CTG	
val gly gly asp leu asp pro ser ser ile-pro asp lys glu gln ala ile ser ala leu	
1240/381	1270/391
CCG GAC TAC GCC AGC CAG CCC GGC AAA CCG CCG CCG GAG GAC CTg aag TAA	
pro asp tyr ala ser gln pro gly lys pro pro arg glu asp leu lys OCH	

FIG.2B

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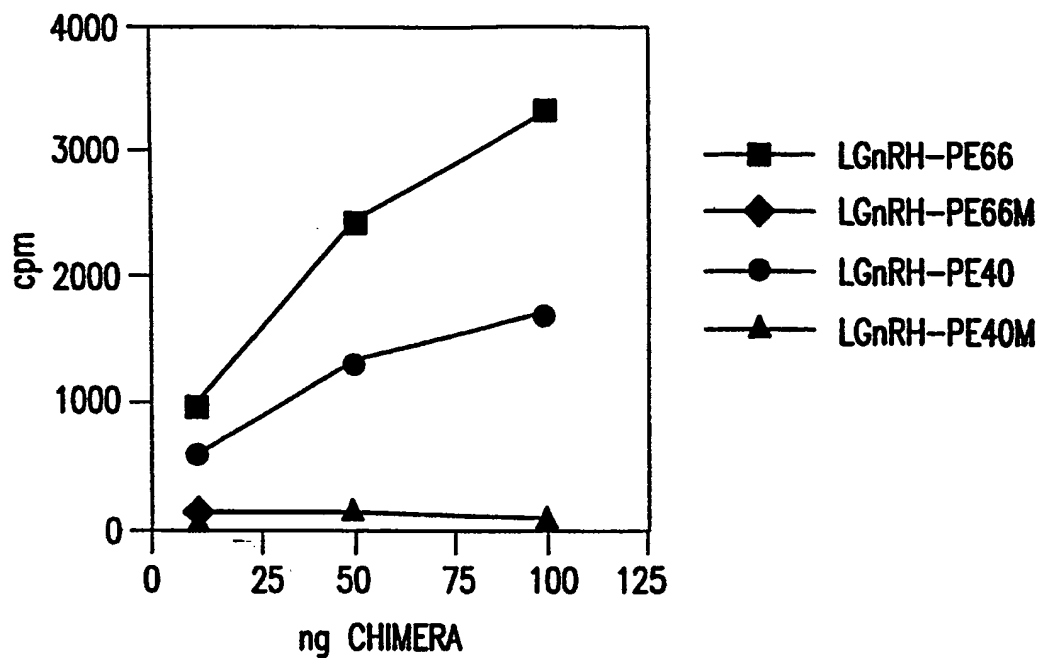


FIG.3

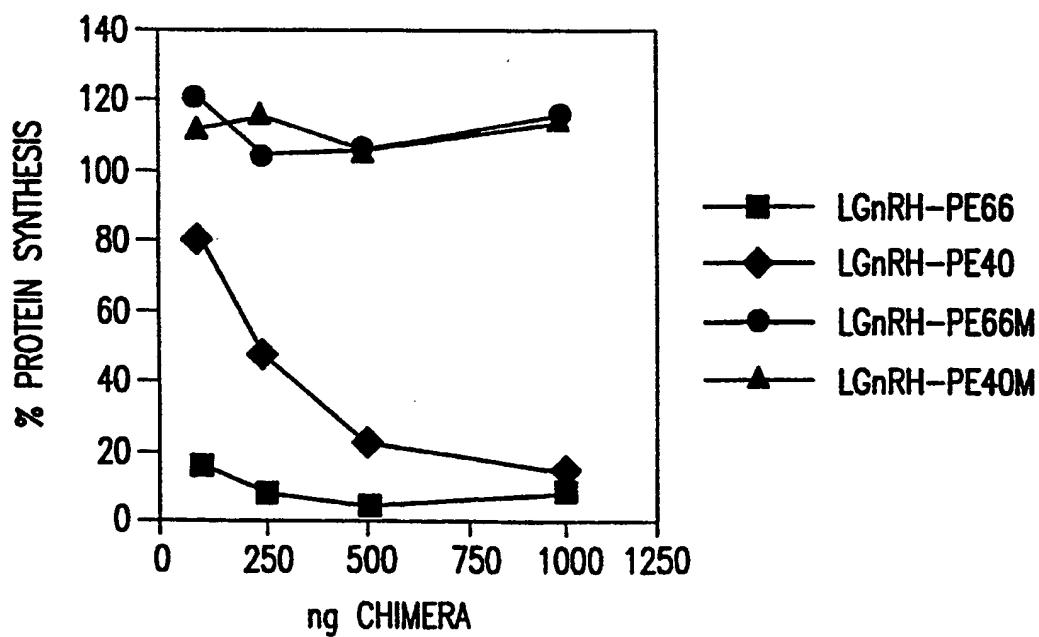


FIG.4

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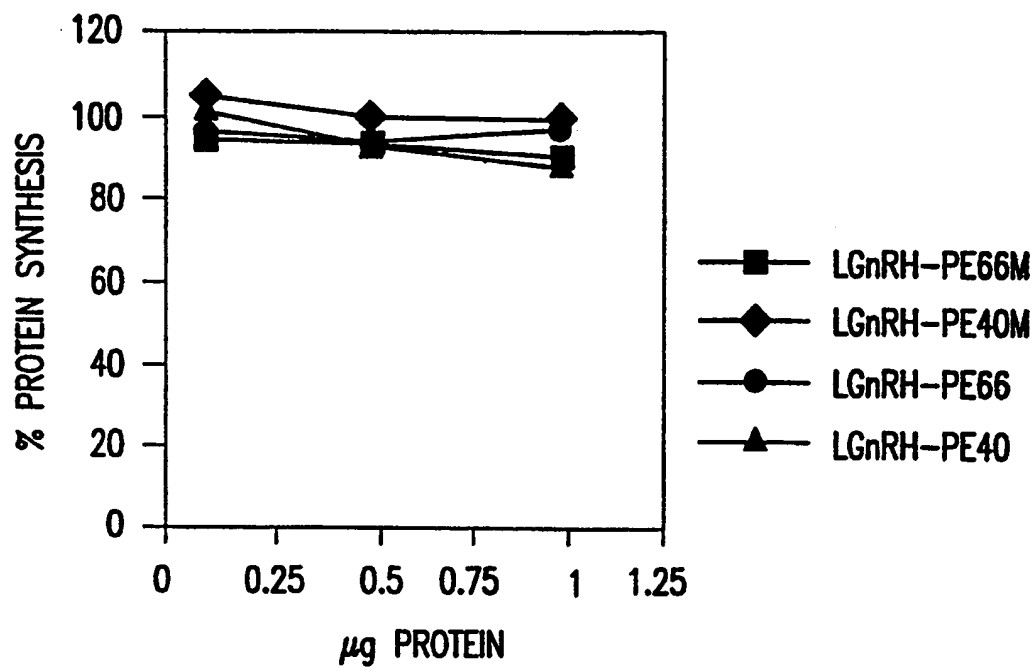


FIG.5

SEQUENCE LISTING

- (1) GENERAL INFORMATION:
- (i) APPLICANT: Yisum Research Development Company of The Hebrew University of Jerusalem
- (ii) TITLE OF INVENTION: METHODS OF CANCER DIAGNOSIS USING A CHIMERIC TOXIN
- (iii) NUMBER OF SEQUENCES: 7
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: Pennie & Edmonds, LLP
- (B) STREET: 1155 Avenue of the Americas
- (C) CITY: New York
- (D) STATE: NY
- (E) COUNTRY: USA
- (F) ZIP: 10036-2811
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Diskette
- (B) COMPUTER: IBM Compatible
- (C) OPERATING SYSTEM: Windows
- (D) SOFTWARE: FastSEQ for Windows Version 2.0b
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER:
- (B) FILING DATE:
- (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: 09/046,992
- (B) FILING DATE: 24-MAR-1998
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Poissant, Brian M
- (B) REGISTRATION NUMBER: 28,462
- (C) REFERENCE/DOCKET NUMBER: 9457-0013-228
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: 650-493-4935
- (B) TELEFAX: 650-493-5556
- (C) TELEX: 66141 PENNIE
- (2) INFORMATION FOR SEQ ID NO:1:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1908 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 1...1905
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG GAG CAC TGG TCC TAT TGG CTG CGC CCT GGA GAA GCT GGA GGA GGA	48
Met Glu His Trp Ser Tyr Trp Leu Arg Pro Gly Glu Ala Gly Gly Gly	
1 5 10 15	
GGA TCC GGA GGA GGA GGA TCC GGT CAA GCT TTC GAC CTC TGG AAC GAA	96
Gly Ser Gly Gly Gly Ser Gly Gln Ala Phe Asp Leu Trp Asn Glu	
20 25 30	
TGC GCC AAA GCC TGC GTG CTC GAC CTC AAG GAC GGC GTG CGT TCC AGC	144
Cys Ala Lys Ala Cys Val Leu Asp Leu Lys Asp Gly Val Arg Ser Ser	
35 40 45	
CGC ATG AGC GTC GAC CCG GCC ATC GCC GAC ACC AAC GGC CAG GGC GTG	192
Arg Met Ser Val Asp Pro Ala Ile Ala Asp Thr Asn Gly Gln Gly Val	
50 55 60	
CTG CAC TAC TCC ATG GTC CTG GAG GGC GGC AAC GAC GCG CTC GAG CTG	240
Leu His Tyr Ser Met Val Leu Glu Gly Gly Asn Asp Ala Leu Glu Leu	
65 70 75 80	
GCC ATC GAC AAC GCC CTC AGC ATC ACC AGC GAC GGC CTG ACC ATC CGC	288
Ala Ile Asp Asn Ala Leu Ser Ile Thr Ser Asp Gly Leu Thr Ile Arg	
85 90 95	
CTC GAA GGC GGC GTC GAG CCG AAC AAG CCG CTG CCG TAC AGC TAC ACG	336
Leu Glu Gly Gly Val Glu Pro Asn Lys Pro Leu Arg Tyr Ser Tyr Thr	
100 105 110	
CGC CAG GCG CGC GGC AGG TGG TCG CTG AAC TGG CTG GTA CCG ATC GGC	384
Arg Gln Ala Arg Gly Arg Trp Ser Leu Asn Trp Leu Val Pro Ile Gly	
115 120 125	
CAC GAG AAG CCC TCG AAC ATC AAG GTG TTC ATC CAC GAA CTG AAC GCC	432
His Glu Lys Pro Ser Asn Ile Lys Val Phe Ile His Glu Leu Asn Ala	
130 135 140	
GGC AAC CAG CTC AGC CAC ATG TCG CCG ATC TAC ACC ATC GAG ATG GGC	480
Gly Asn Gln Leu Ser His Met Ser Pro Ile Tyr Thr Ile Glu Met Gly	
145 150 155 160	
GAC GAG TTG CTG GCG AAG CTG GCG CGC GAT GCC ACC TTC TTC GTC AGG	528
Asp Glu Leu Leu Ala Lys Leu Ala Arg Asp Ala Thr Phe Phe Val Arg	
165 170 175	
GCG CAC GAG AGC AAC GAG ATG CAG CCG ACG CTC GCC ATC AGC CAT GCC	576

Ala His Glu Ser Asn Glu Met Gln Pro Thr Leu Ala Ile Ser His Ala	
180 185 190	
GGG GTC AGC GTG GTC ATG GCC CAG AAC CAG CCG CGC CGG GAA AAG CGC	624
Gly Val Ser Val Val Met Ala Gln Asn Gln Pro Arg Arg Glu Lys Arg	
195 200 205	
TGG AGC GAA TGG GCC AGC GGC AAG GTG TTG TGC CTG CTC GAC CCG CTG	672
Trp Ser Glu Trp Ala Ser Gly Lys Val Leu Cys Leu Leu Asp Pro Leu	
210 215 220	
GAC GGG GTC TAC AAC TAC CTC GCC CAG CAA CGC TGC AAC CTC GAC GAT	720
Asp Gly Val Tyr Asn Tyr Leu Ala Gln Gln Arg Cys Asn Leu Asp Asp	
225 230 235 240	
ACC TGG GAA GGC AAG ATC TAC CCG GTG CTC GCC GGC AAC CCG GCG AAG	768
Thr Trp Glu Gly Lys Ile Tyr Arg Val Leu Ala Gly Asn Pro Ala Lys	
245 250 255	
CAT GAC CTG GAC ATC AAA CCC ACG GTC ATC AGT GAA GAG CTG GAG TTT	816
His Asp Leu Asp Ile Lys Pro Thr Val Ile Ser Glu Glu Leu Glu Phe	
260 265 270	
CCC GAG GGC GGC AGC CTG GCC GCG CTG ACC GCG CAC CAG GCT TGC CAC	864
Pro Glu Gly Gly Ser Leu Ala Ala Leu Thr Ala His Gln Ala Cys His	
275 280 285	
CTG CCG CTG GAG ACT TTC ACC CGT CAT CGC CAG CCG CGC GGC TGG GAA	912
Leu Pro Leu Glu Thr Phe Thr Arg His Arg Gln Pro Arg Gly Trp Glu	
290 295 300	
CAA CTG GAG CAG TGC GGC TAT CCG GTG CAG CCG CTG GTC GCC CTC TAC	960
Gln Leu Glu Gln Cys Gly Tyr Pro Val Gln Arg Leu Val Ala Leu Tyr	
305 310 315 320	
CTG GCG GCG CCG CTG TCG TGG AAC CAG GTC GAC CAG GTG ATC CGC AAC	1008
Leu Ala Ala Arg Leu Ser Trp Asn Gln Val Asp Gln Val Ile Arg Asn	
325 330 335	
GCC CTG GCC AGC CCC GGC AGC GGC GGC GAC CTG GGC GAA GCG ATC CGC	1056
Ala Leu Ala Ser Pro Gly Ser Gly Gly Asp Leu Gly Glu Ala Ile Arg	
340 345 350	
GAG CAG CCG GAG CAG GCC CGT CTG GCC CTG ACC CTG GCC GCC GCC GAG	1104
Glu Gln Pro Glu Gln Ala Arg Leu Ala Leu Thr Leu Ala Ala Ala Glu	
355 360 365	
AGC GAG CGC TTC GTC CCG CAG GGC ACC GGC AAC GAC GAG GCC GGC GCG	1152
Ser Glu Arg Phe Val Arg Gln Gly Thr Gly Asn Asp Glu Ala Gly Ala	
370 375 380	
GCC AAC GCC GAC GTG GTG AGC CTG ACC TGC CCG GTC GCC GCC GGT GAA	1200
Ala Asn Ala Asp Val Val Ser Leu Thr Cys Pro Val Ala Ala Gly Glu	
385 390 395 400	
TGC GCG GGC CCG GCG GAC AGC GGC GAC GCC CTG CTG GAG GCG AAC TAT	1248

Cys	Ala	Gly	Pro	Ala	Asp	Ser	Gly	Asp	Ala	Leu	Leu	Glu	Ala	Asn	Tyr		
				405					410					415			
CCC	ACT	GGC	GCG	GAG	TTC	CTC	GGC	GAC	GGC	GAC	GTC	AGC	TTC	AGC		1296	
Pro	Thr	Gly	Ala	Glu	Phe	Leu	Gly	Asp	Gly	Gly	Asp	Val	Ser	Phe	Ser		
			420					425					430				
ACC	CGC	GGC	ACG	CAG	AAC	TGG	ACG	GTG	GAG	CGG	CTG	CTC	CAG	GCG	CAC		1344
Thr	Arg	Gly	Thr	Gln	Asn	Trp	Thr	Val	Glu	Arg	Leu	Leu	Gln	Ala	His		
			435					440					445				
CGC	CAA	CTG	GAG	GAG	CGC	GGC	TAT	GTG	TTC	GTC	GGC	TAC	CAC	GGC	ACC		1392
Arg	Gln	Leu	Glu	Glu	Arg	Gly	Tyr	Val	Phe	Val	Gly	Tyr	His	Gly	Thr		
			450				455					460					
TTC	CTC	GAA	GCG	GCG	CAA	AGC	ATC	GTC	TTC	GGC	GGG	GTG	CGC	GCG	CGC		1440
Phe	Leu	Glu	Ala	Ala	Gln	Ser	Ile	Val	Phe	Gly	Gly	Val	Arg	Ala	Arg		
			465				470					475			480		
AGC	CAG	GAC	CTC	GAC	GCG	ATC	TGG	CGC	GGT	TTC	TAT	ATC	GCC	GGC	GAT		1488
Ser	Gln	Asp	Leu	Asp	Ala	Ile	Trp	Arg	Gly	Phe	Tyr	Ile	Ala	Gly	Asp		
				485					490					495			
CCG	GCG	CTG	GCC	TAC	GGC	TAC	GCC	CAG	GAC	CAG	GAA	CCC	GAC	GCA	CGC		1536
Pro	Ala	Leu	Ala	Tyr	Gly	Tyr	Ala	Gln	Asp	Gln	Glu	Pro	Asp	Ala	Arg		
			500					505					510				
GGC	CGG	ATC	CGC	AAC	GGT	GCC	CTG	CTG	CGG	GTC	TAT	GTG	CCG	CGC	TCG		1584
Gly	Arg	Ile	Arg	Asn	Gly	Ala	Leu	Leu	Arg	Val	Tyr	Val	Pro	Arg	Ser		
			515				520						525				
AGC	CTG	CCG	GGC	TTC	TAC	CGC	ACC	AGC	CTG	ACC	CTG	GCC	GCG	CCG	GAG		1632
Ser	Leu	Pro	Gly	Phe	Tyr	Arg	Thr	Ser	Leu	Thr	Leu	Ala	Ala	Pro	Glu		
			530				535					540					
GCG	GCG	GGC	GAG	GTC	GAA	CGG	CTG	ATC	GGC	CAT	CCG	CTG	CCG	CTG	CGC		1680
Ala	Ala	Gly	Glu	Val	Glu	Arg	Leu	Ile	Gly	His	Pro	Leu	Pro	Leu	Arg		
			545			550				555					560		
CTG	GAC	GCC	ATC	ACC	GGC	CCC	GAG	GAG	GAA	GGC	GGG	CGC	CTG	GAG	ACC		1728
Leu	Asp	Ala	Ile	Thr	Gly	Pro	Glu	Glu	Glu	Gly	Gly	Arg	Leu	Glu	Thr		
				565					570					575			
ATT	CTC	GGC	TGG	CCG	CTG	GCC	GAG	CGC	ACC	GTG	GTG	ATT	CCC	TCG	GCG		1776
Ile	Leu	Gly	Trp	Pro	Leu	Ala	Glu	Arg	Thr	Val	Val	Ile	Pro	Ser	Ala		
			580					585					590				
ATC	CCC	ACC	GAC	CCG	CGC	AAC	GTC	GGC	GGC	GAC	CTC	GAC	CCG	TCC	AGC		1824
Ile	Pro	Thr	Asp	Pro	Arg	Asn	Val	Gly	Gly	Asp	Leu	Asp	Pro	Ser	Ser		
			595				600					605					
ATC	CCC	GAC	AAG	GAA	CAG	GCG	ATC	AGC	GCC	CTG	CCG	GAC	TAC	GCC	AGC		1872
Ile	Pro	Asp	Lys	Glu	Gln	Ala	Ile	Ser	Ala	Leu	Pro	Asp	Tyr	Ala	Ser		
			610				615					620					
CAG	CCC	GGC	AAA	CCG	CCG	CGC	GAG	GAC	CTG	AAG	TAA						1908

Gln Pro Gly Lys Pro Pro Arg Glu Asp Leu Lys
625 630 635

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 635 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Met Glu His Trp Ser Tyr Trp Leu Arg Pro Gly Glu Ala Gly Gly Gly
 1           5           10           15
Gly Ser Gly Gly Gly Ser Gly Gln Ala Phe Asp Leu Trp Asn Glu
 20           25           30
Cys Ala Lys Ala Cys Val Leu Asp Leu Lys Asp Gly Val Arg Ser Ser
 35           40           45
Arg Met Ser Val Asp Pro Ala Ile Ala Asp Thr Asn Gly Gln Gly Val
 50           55           60
Leu His Tyr Ser Met Val Leu Glu Gly Gly Asn Asp Ala Leu Glu Leu
 65           70           75           80
Ala Ile Asp Asn Ala Leu Ser Ile Thr Ser Asp Gly Leu Thr Ile Arg
 85           90           95
Leu Glu Gly Gly Val Glu Pro Asn Lys Pro Leu Arg Tyr Ser Tyr Thr
100           105           110
Arg Gln Ala Arg Gly Arg Trp Ser Leu Asn Trp Leu Val Pro Ile Gly
115           120           125
His Glu Lys Pro Ser Asn Ile Lys Val Phe Ile His Glu Leu Asn Ala
130           135           140
Gly Asn Gln Leu Ser His Met Ser Pro Ile Tyr Thr Ile Glu Met Gly
145           150           155           160
Asp Glu Leu Leu Ala Lys Leu Ala Arg Asp Ala Thr Phe Phe Val Arg
165           170           175
Ala His Glu Ser Asn Glu Met Gln Pro Thr Leu Ala Ile Ser His Ala
180           185           190
Gly Val Ser Val Val Met Ala Gln Asn Gln Pro Arg Arg Glu Lys Arg
195           200           205
Trp Ser Glu Trp Ala Ser Gly Lys Val Leu Cys Leu Leu Asp Pro Leu
210           215           220
Asp Gly Val Tyr Asn Tyr Leu Ala Gln Gln Arg Cys Asn Leu Asp Asp
225           230           235           240
Thr Trp Glu Gly Lys Ile Tyr Arg Val Leu Ala Gly Asn Pro Ala Lys
245           250           255
His Asp Leu Asp Ile Lys Pro Thr Val Ile Ser Glu Glu Leu Glu Phe
260           265           270
Pro Glu Gly Gly Ser Leu Ala Ala Leu Thr Ala His Gln Ala Cys His
275           280           285
Leu Pro Leu Glu Thr Phe Thr Arg His Arg Gln Pro Arg Gly Trp Glu
290           295           300
Gln Leu Glu Gln Cys Gly Tyr Pro Val Gln Arg Leu Val Ala Leu Tyr

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305          310          315          320
Leu Ala Ala Arg Leu Ser Trp Asn Gln Val Asp Gln Val Ile Arg Asn
          325          330          335
Ala Leu Ala Ser Pro Gly Ser Gly Gly Asp Leu Gly Glu Ala Ile Arg
          340          345          350
Glu Gln Pro Glu Gln Ala Arg Leu Ala Leu Thr Leu Ala Ala Ala Glu
          355          360          365
Ser Glu Arg Phe Val Arg Gln Gly Thr Gly Asn Asp Glu Ala Gly Ala
          370          375          380
Ala Asn Ala Asp Val Val Ser Leu Thr Cys Pro Val Ala Ala Gly Glu
385          390          395          400
Cys Ala Gly Pro Ala Asp Ser Gly Asp Ala Leu Leu Glu Ala Asn Tyr
          405          410          415
Pro Thr Gly Ala Glu Phe Leu Gly Asp Gly Gly Asp Val Ser Phe Ser
          420          425          430
Thr Arg Gly Thr Gln Asn Trp Thr Val Glu Arg Leu Leu Gln Ala His
          435          440          445
Arg Gln Leu Glu Glu Arg Gly Tyr Val Phe Val Gly Tyr His Gly Thr
          450          455          460
Phe Leu Glu Ala Ala Gln Ser Ile Val Phe Gly Gly Val Arg Ala Arg
465          470          475          480
Ser Gln Asp Leu Asp Ala Ile Trp Arg Gly Phe Tyr Ile Ala Gly Asp
          485          490          495
Pro Ala Leu Ala Tyr Gly Tyr Ala Gln Asp Gln Glu Pro Asp Ala Arg
          500          505          510
Gly Arg Ile Arg Asn Gly Ala Leu Leu Arg Val Tyr Val Pro Arg Ser
          515          520          525
Ser Leu Pro Gly Phe Tyr Arg Thr Ser Leu Thr Leu Ala Ala Pro Glu
          530          535          540
Ala Ala Gly Glu Val Glu Arg Leu Ile Gly His Pro Leu Pro Leu Arg
545          550          555          560
Leu Asp Ala Ile Thr Gly Pro Glu Glu Glu Gly Gly Arg Leu Glu Thr
          565          570          575
Ile Leu Gly Trp Pro Leu Ala Glu Arg Thr Val Val Ile Pro Ser Ala
          580          585          590
Ile Pro Thr Asp Pro Arg Asn Val Gly Gly Asp Leu Asp Pro Ser Ser
          595          600          605
Ile Pro Asp Lys Glu Gln Ala Ile Ser Ala Leu Pro Asp Tyr Ala Ser
          610          615          620
Gln Pro Gly Lys Pro Pro Arg Glu Asp Leu Lys
625          630          635

```

(2) INFORMATION FOR SEQ ID NO.3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1191 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...1188
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATG GAG CAC TGG TCC TAT TGG CTG CGC CCT GGA GAA GCT GGA GGA GGA	48
Met Glu His Trp Ser Tyr Trp Leu Arg Pro Gly Glu Ala Gly Gly Gly	
1 5 10 15	
GGA TCC GGA GGA GGA GGA TCC GGT CAA GCT TTT GTT AAC GCC CAT ATG	96
Gly Ser Gly Gly Gly Gly Ser Gly Gln Ala Phe Val Asn Ala His Met	
20 25 30	
GCC GAA GAG GGC GGC AGC CTG GCC GCG CTG ACC GCG CAC CAG GCT TGC	144
Ala Glu Glu Gly Gly Ser Leu Ala Ala Leu Thr Ala His Gln Ala Cys	
35 40 45	
CAC CTG CCG CTG GAG ACT TTC ACC CGT CAT CGC CAG CCG CCG GGC TGG	192
His Leu Pro Leu Glu Thr Phe Thr Arg His Arg Gln Pro Arg Gly Trp	
50 55 60	
GAA CAA CTG GAG CAG TGC GGC TAT CCG GTG CAG CCG CTG GTC GCC CTC	240
Glu Gln Leu Glu Gln Cys Gly Tyr Pro Val Gln Arg Leu Val Ala Leu	
65 70 75 80	
TAC CTG GCG CCG CCG CTG TCG TGG AAC CAG GTC GAC CAG GTC ATC CGC	288
Tyr Leu Ala Ala Arg Leu Ser Trp Asn Gln Val Asp Gln Val Ile Arg	
85 90 95	
AAC GCC CTG GCC AGC CCC GGC AGC GGC GGC GAC CTG GGC GAA GCG ATC	336
Asn Ala Leu Ala Ser Pro Gly Ser Gly Gly Asp Leu Gly Glu Ala Ile	
100 105 110	
CGC GAG CAG CCG GAG CAG GCC CGT CTG GCC CTG ACC CTG GCC GCC GCC	384
Arg Glu Gln Pro Glu Gln Ala Arg Leu Ala Leu Thr Leu Ala Ala Ala	
115 120 125	
GAG AGC GAG CCG TTC GTC CCG CAG GGC ACC GGC AAC GAC GAG GCC GGC	432
Glu Ser Glu Arg Phe Val Arg Gln Gly Thr Gly Asn Asp Glu Ala Gly	
130 135 140	
GCG GCC AAC GCC GAC GTG GTG AGC CTG ACC TGC CCG GTC GCC GCC GGT	480
Ala Ala Asn Ala Asp Val Val Ser Leu Thr Cys Pro Val Ala Ala Gly	
145 150 155 160	
GAA TGC GCG GGC CCG GCG GAC AGC GCG GAC GCC CTG CTG GAG CCG AAC	528
Glu Cys Ala Gly Pro Ala Asp Ser Gly Asp Ala Leu Leu Glu Arg Asn	
165 170 175	
TAT CCC ACT GGC GCG GAG TTC CTC GGC GAC GGC GGC GAC GTC AGC TTC	576
Tyr Pro Thr Gly Ala Glu Phe Leu Gly Asp Gly Gly Asp Val Ser Phe	
180 185 190	
AGC ACC CCG GGC ACG CAG AAC TGG ACG GTG GAG CCG CTG CTC CAG GCG	624
Ser Thr Arg Gly Thr Gln Asn Trp Thr Val Glu Arg Leu Leu Gln Ala	
195 200 205	
CAC CCG CAA CTG GAG GAG CCG GGC TAT GTG TTC GTC GGC TAC CAC GGC	672
His Arg Gln Leu Glu Glu Arg Gly Tyr Val Phe Val Gly Tyr His Gly	

210	215	220	
ACC TTC CTC GAA GCG GCG CAA AGC ATC GTC TTC GGC GGC GTG CGC GCG			720
Thr Phe Leu Glu Ala Ala Gln Ser Ile Val Phe Gly Gly Val Arg Ala			
225	230	235	240
CGC AGC CAG GAC CTC GAC GCG ATC TGG CGC GGT TTC TAT ATC GCC GCG			768
Arg Ser Gln Asp Leu Asp Ala Ile Trp Arg Gly Phe Tyr Ile Ala Gly			
245	250		255
GAT CCG GCG CTG GCC TAC GGC TAC GCC CAG GAC CAG GAA CCC GAC GCA			816
Asp Pro Ala Leu Ala Tyr Gly Tyr Ala Gln Asp Gln Glu Pro Asp Ala			
260	265		270
CGC GGC CGG ATC CGC AAC GGT GCC CTG CTG CGG GTC TAT GTG CCG CGC			864
Arg Gly Arg Ile Arg Asn Gly Ala Leu Leu Arg Val Tyr Val Pro Arg			
275	280		285
TCG AGC CTG CCG GGC TTC TAC CGC ACC AGC CTG ACC CTG GCC GCG CCG			912
Ser Ser Leu Pro Gly Phe Tyr Arg Thr Ser Leu Thr Leu Ala Ala Pro			
290	295		300
GAG GCG GCG GGC GAG GTC GAA CGG CTG ATC GGC CAT CCG CTG CCG CTG			960
Glu Ala Ala Gly Glu Val Glu Arg Leu Ile Gly His Pro Leu Pro Leu			
305	310	315	320
CGC CTG GAC GCC ATC ACC GGC CCC GAG GAG GAA GGC GGG CGC CTG GAG			1008
Arg Leu Asp Ala Ile Thr Gly Pro Glu Glu Glu Gly Gly Arg Leu Glu			
325	330		335
ACC ATT CTC GGC TGG CCG CTG GCC GAG CGC ACC GTG GTG ATT CCC TCG			1056
Thr Ile Leu Gly Trp Pro Leu Ala Glu Arg Thr Val Val Ile Pro Ser			
340	345		350
GCG ATC CCC ACC GAC CCG CGC AAC GTC GGC GGC GAC CTC GAC CCG TCC			1104
Ala Ile Pro Thr Asp Pro Arg Asn Val Gly Gly Asp Leu Asp Pro Ser			
355	360		365
AGC ATC CCC GAC AAG GAA CAG GCG ATC AGC GCC CTG CCG GAC TAC GCC			1152
Ser Ile Pro Asp Lys Glu Gln Ala Ile Ser Ala Leu Pro Asp Tyr Ala			
370	375		380
AGC CAG CCC GGC AAA CCG CCG CGC GAG GAC CTG AAG TAA			1191
Ser Gln Pro Gly Lys Pro Pro Arg Glu Asp Leu Lys			
385	390		395

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```

Met Glu His Trp Ser Tyr Trp Leu Arg Pro Gly Glu Ala Gly Gly Gly
 1      5      10      15
Gly Ser Gly Gly Gly Ser Gly Gln Ala Phe Val Asn Ala His Met
 20      25      30
Ala Glu Glu Gly Gly Ser Leu Ala Ala Leu Thr Ala His Gln Ala Cys
 35      40      45
His Leu Pro Leu Glu Thr Phe Thr Arg His Arg Gln Pro Arg Gly Trp
 50      55      60
Glu Gln Leu Glu Gln Cys Gly Tyr Pro Val Gln Arg Leu Val Ala Leu
 65      70      75      80
Tyr Leu Ala Ala Arg Leu Ser Trp Asn Gln Val Asp Gln Val Ile Arg
 85      90      95
Asn Ala Leu Ala Ser Pro Gly Ser Gly Gly Asp Leu Gly Glu Ala Ile
100      105      110
Arg Glu Gln Pro Glu Gln Ala Arg Leu Ala Leu Thr Leu Ala Ala Ala
115      120      125
Glu Ser Glu Arg Phe Val Arg Gln Gly Thr Gly Asn Asp Glu Ala Gly
130      135      140
Ala Ala Asn Ala Asp Val Val Ser Leu Thr Cys Pro Val Ala Ala Gly
145      150      155      160
Glu Cys Ala Gly Pro Ala Asp Ser Gly Asp Ala Leu Leu Glu Arg Asn
165      170      175
Tyr Pro Thr Gly Ala Glu Phe Leu Gly Asp Gly Gly Asp Val Ser Phe
180      185      190
Ser Thr Arg Gly Thr Gln Asn Trp Thr Val Glu Arg Leu Leu Gln Ala
195      200      205
His Arg Gln Leu Glu Glu Arg Gly Tyr Val Phe Val Gly Tyr His Gly
210      215      220
Thr Phe Leu Glu Ala Ala Gln Ser Ile Val Phe Gly Gly Val Arg Ala
225      230      235      240
Arg Ser Gln Asp Leu Asp Ala Ile Trp Arg Gly Phe Tyr Ile Ala Gly
245      250      255
Asp Pro Ala Leu Ala Tyr Gly Tyr Ala Gln Asp Gln Glu Pro Asp Ala
260      265      270
Arg Gly Arg Ile Arg Asn Gly Ala Leu Leu Arg Val Tyr Val Pro Arg
275      280      285
Ser Ser Leu Pro Gly Phe Tyr Arg Thr Ser Leu Thr Leu Ala Ala Pro
290      295      300
Glu Ala Ala Gly Glu Val Glu Arg Leu Ile Gly His Pro Leu Pro Leu
305      310      315      320
Arg Leu Asp Ala Ile Thr Gly Pro Glu Glu Gly Gly Arg Leu Glu
325      330      335
Thr Ile Leu Gly Trp Pro Leu Ala Glu Arg Thr Val Val Ile Pro Ser
340      345      350
Ala Ile Pro Thr Asp Pro Arg Asn Val Gly Gly Asp Leu Asp Pro Ser
355      360      365
Ser Ile Pro Asp Lys Glu Gln Ala Ile Ser Ala Leu Pro Asp Tyr Ala
370      375      380
Ser Gln Pro Gly Lys Pro Pro Arg Glu Asp Leu Lys
385      390      395

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(2) INFORMATION FOR SEQ ID NO:5:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Gly Gly Gly Gly Ser
 1 5

(2) INFORMATION FOR SEQ ID NO:6:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Glu Gly Lys Ser Ser Gly Ser Gly Ser Glu Ser Lys Val Asp
 1 5 10

(2) INFORMATION FOR SEQ ID NO:7:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Lys Glu Ser Gly Ser Val Ser Ser Glu Gln Leu Ala Gln Phe Arg Ser
 1 5 10 15
 Leu Asp